

SEQUENCE LISTING

<110> Broze, George J., Jr.

<120> Protein Z-Dependent Protease Inhibitor

<130> WU-3110/1

<150> US 60/086,571

<151> 1998-05-19

<160> 16

<170> Word Perfect 5.0

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<213> Artificial Sequence

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Leu Ala Pro Ser Pro Gln Ser Pro Glu Xaa Xaa Ala
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Arg Tyr Lys Gly Gly Ser Pro Xaa Ile Ser Gln Pro Xaa Leu
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Asp Phe Asp Val

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Gln Asp Lys Leu Gln Glu Gln Glu Gly Ser Leu Ala Ala Glu Gly
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Arg His Ser Leu Ala Ser Ala Ala Asp His
 35 40

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 cagggatgtg tgctgtccca gggctgagaa gtggcagggtg agctggtgat 200
 tccttactgc ccaggttcgt tctaggaagg tgcgtcctca ccatgctgga 250

tgggtgccta gtccaggagc accccctgag ctccctggcct agactccaaa 300
 ggggtgggta gatgagcaaa gactttacaa agaccttagg cgatatatgt 350
 ccaggagcac ccaggaatta ctgggctacc actgcagact gcaggacaag 400
 ctccaagaac aggaaggaag tcttgacgct gaaggaggagc actccttggc 450
 ctccgcagcc gat cac atg aag gtg gtg cca agt ctc ctg ctc 493
 Met Lys Val Val Pro Ser Leu Leu Leu
 -20 -15
 tcc gtc ctc ctg gca cag gtg tgg ctg gta ccc ggc ttg gcc 535
 Ser Val Leu Leu Ala Lys Val Trp Leu Val Pro Gly Leu Ala
 -10 -5 -1 1
 ccc agt cct cag tgc cca gag acc cca gcc cct cag aac cag 577
 Pro Ser Pro Gln Ser Pro Glu Thr Pro Ala Pro Gln Asn Gln
 5 10 15
 acc agc agg gta gtg cag gct ccc aag gag gaa gag gaa gat 619
 Thr Ser Arg Val Gln Ala Pro Lys Glu Glu Glu Glu Glu Asp
 20 25 30
 gag cag gag gcc agc gag gag aag gcc agt gag gaa gag aaa 661
 Glu Gln Glu Ala Ser Glu Glu Lys Ala Ser Glu Glu Glu Lys
 35 40
 gcc tgg ctg atg gcc agc agg cag cag ctt gcc aag gag act 703
 Ala Trp Leu Met Ala Ser Arg Gln Gln Leu Ala Lys Glu Thr
 45 50 55
 tca aac ttc gga ttc agc ctg ctg cga aag atc tcc atg agg 745
 Ser Asn Phe Gly Phe Ser Leu Leu Arg Lys Ile Ser Met Arg
 60 65 70
 cac gat ggc aac atg gtc ttc tct cca ttt ggc atg tcc ttg 787
 His Asp Gly Asn Met Val Phe Ser Pro Phe Gly Met Ser Leu
 75 80 85
 gcc atg aca ggc ttg atg ctg ggg gcc aca ggg ccg act gaa 829
 Ala Met Thr Gly Leu Met Leu Gly Ala Thr Gly Pro Thr Glu
 90 95 100
 acc cag atc aag aga ggg ctc cac ttg cag gcc ctg aag ccc 871
 Thr Gln Ile Lys Arg Gly Leu His Leu Gln Ala Leu Lys Pro
 105 110
 acc aag ccc ggg ctc ctg cct tcc ctc ttt aag gga ctc aga 913
 Thr Lys Pro Gly Leu Leu Pro Ser Leu Phe Lys Gly Leu Arg
 115 120 125

20070724 014002

gag acc ctc tcc cgc aac ctg gaa ctg ggc ctc aca cag ggg	955
Glu Thr Leu Ser Arg Asn Leu Glu Leu Gly Leu Thr Gln Gly	
130 135 140	
agt ttt gcc ttc atc cac aag gat ttt gat gtc aaa gag act	997
Ser Phe Ala Phe Ile His Lys Asp Phe Asp Val Lys Glu Thr	
145 150 155	
ttc ttc aat tta tcc aag agg tat ttt gat aca gag tgc gtg	1039
Phe Phe Asn Leu Ser Lys Arg Tyr Phe Asp Thr Glu Cys Val	
160 165 170	
cct atg aat ttt cgc aat gcc tca cag gcc aaa agg ctc atg	1081
Pro Met Asn Phe Arg Asn Ala Ser Gln Ala Lys Arg Leu Met	
175 180	
aat cat tac att aac aaa gag act cgg ggg aaa att ccc aaa	1123
Asn His Tyr Ile Asn Lys Glu Thr Arg Gly Lys Ile Pro Lys	
185 190 195	
ctg ttt gat gag att aat cct gaa acc aaa tta att ctt gtg	1165
Leu Phe Asp Glu Ile Asn Pro Glu Thr Lys Leu Ile Leu Val	
200 205 210	
gat tac atc ttg ttc aaa ggg aaa tgg ttg acc cca ttt gac	1207
Asp Tyr Ile Leu Phe Lys Gly Lys Trp Leu Thr Pro Phe Asp	
215 220 225	
cct gtc ttc acc gaa gtc gac act ttc cac ctg gac aag tac	1249
Pro Val Phe Thr Glu Val Asp Thr Phe His Leu Asp Lys Tyr	
230 235 240	
aag acc att aag gtg ccc atg atg tac ggt gca ggc aag ttt	1291
Lys Thr Ile Lys Val Pro Met Met Tyr Gly Ala Gly Lys Phe	
245 250	
gcc tcc acc ttt gac aag aat ttt cgt tgt cat gtc ctc aaa	1333
Ala Ser Thr Phe Asp Lys Asn Phe Arg Cys His Val Leu Lys	
255 260 265	
ctg ccc tac caa gga aat gcc acc atg ctg gtg gtc ctc atg	1375
Leu Pro Tyr Gln Gly Asn Ala Thr Met Leu Val Val Leu Met	
270 275 280	
gag aaa atg ggt gac cac ctc gcc ctt gaa gac tac ctg acc	1417
Glu Lys Met Gly Asp His Leu Ala Leu Glu Asp Tyr Leu Thr	
285 290 295	
aca gac ttg gtg gag aca tgg ctc aga aac atg aaa acc aga	1459
Thr Asp Leu Val Glu Thr Trp Leu Arg Asn Met Lys Thr Arg	
300 305 310	

aac atg gaa gtt ttc ttt ccg aag ttc aag cta gat cag aag 1501
 Asn Met Glu Val Phe Phe Pro Lys Phe Lys Leu Asp Gln Lys
 315 320

tat gag atg cat gag ctg ctt agg cag atg gga atc aga aga 1543
 Tyr Glu Met His Glu Leu Leu Arg Gln Met Gly Ile Arg Arg
 325 330 335

atc ttc tca ccc ttt gct gac ctt agt gaa ctc tca gct act 1585
 Ile Phe Ser Pro Phe Ala Asp Leu Ser Glu Leu Ser Ala Thr
 340 345 350

gga aga aat ctc caa gta tcc agg gtt tta caa aga aca gtg 1627
 Gly Arg Asn Leu Gln Val Ser Arg Val Leu Gln Arg Thr Val
 355 360 365

att gaa gtt gat gaa agg ggc act gag gca gtg gca gga atc 1669
 Ile Glu Val Asp Glu Arg Gly Thr Glu Ala Val Ala Gly Ile
 370 375 380

ttg tca gaa att act gct tat tcc atg cct cct gtc atc aaa 1711
 Leu Ser Glu Ile Thr Ala Tyr Ser Met Pro Pro Val Ile Lys
 385 390

gtg gac cgg cca ttt cat ttc atg atc tat gaa gaa acc tct 1753
 Val Asp Arg Pro Phe His Phe Met Ile Tyr Glu Glu Thr Ser
 395 400 405

gga atg ctt ctg ttt ctg ggc agg gtg gtg aat ccg act ctc 1795
 Gly Met Leu Leu Phe Leu Gly Arg Val Val Asn Pro Thr Leu
 410 415 420

cta taa ttcaggacac gcataagcac ttcgcgtgta gtagatgctg 1841
 Leu 423

aatctgaggt atcaaacaca cacaggatac cagcaatgga tggcagggga 1891

gagtgttcct tttgtttctta actagtttag ggtgtttctca aataaataca 1941

gtagtcccca cttatctgag ggggatacat tcaaagaccc ccagcagatg 1991

cctgaaacgg tggacagtgc tgaaccttat atatattttt tcctacacat 2041

acatacctat gataaagttt aatttataaa ttaggcacag taagagatta 2091

acaataataa caacattaag taaaatgagt tacttgaatg caagcactgc 2141

aataccataa cagtcaaact gattatagag aaggctacta agtgactcat 2191

gggcgaggag catagacagt gtggagacat tgggcaaggg gagaattcac 2241

atcctgggtg ggacagagca ggacaatgca agattccatc ccactactca 2291

gaatggcatg ctgcttaaga cttttagatt gtttatttct ggaatttttc 2341
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 -5 -1 1 5
 Pro Glu Thr Pro Ala Pro Gln Asn Gln Thr Ser Arg Val Val
 10 15 20
 Gln Ala Pro Lys Glu Glu Glu Glu Asp Glu Gln Glu Ala Ser
 25 30 35
 Glu Glu Lys Ala Ser Glu Glu Glu Lys Ala Trp Leu Met Ala
 40 45
 Ser Arg Gln Gln Leu Ala Lys Glu Thr Ser Asn Phe Gly Phe
 50 55 60
 Ser Leu Leu Arg Lys Ile Ser Met Arg His Asp Gly Asn Met
 65 70 75
 Val Phe Ser Pro Phe Gly Met Ser Leu Ala Met Thr Gly Leu
 80 85 90
 Met Leu Gly Ala Thr Gly Pro Thr Glu Thr Gln Ile Lys Arg
 95 100 105
 Gly Leu His Leu Gln Ala Leu Lys Pro Thr Lys Pro Gly Leu
 110 115
 Leu Pro Ser Leu Phe Lys Gly Leu Arg Glu Thr Leu Ser Arg
 120 125 130
 Asn Leu Glu Leu Gly Leu Thr Gln Gly Ser Phe Ala Phe Ile
 135 140 145
 His Lys Asp Phe Asp Val Lys Glu Thr Phe Phe Asn Leu Ser
 150 155 160

Lys Arg Tyr Phe Asp Thr Glu Cys Val Pro Met Asn Phe Arg
 165 170 175
 Asn Ala Ser Gln Ala Lys Arg Leu Met Asn His Tyr Ile Asn
 180 185
 Lys Glu Thr Arg Gly Lys Ile Pro Lys Leu Phe Asp Glu Ile
 190 195 200
 Asn Phe Glu Thr Lys Leu Ile Leu Val Asp Tyr Ile Leu Phe
 205 210 215
 Lys Gly Lys Trp Leu Thr Pro Phe Asp Pro Val Phe Thr Glu
 220 225 230
 Val Asp Thr Phe His Leu Asp Lys Tyr Lys Thr Ile Lys Val
 235 240 245
 Pro Met Met Tyr Gly Ala Gly Lys Phe Ala Ser Thr Phe Asp
 250 255
 Lys Asn Phe Arg Cys His Val Leu Lys Leu Pro Tyr Gln Gly
 260 265 270
 Asn Ala Thr Met Leu Val Val Leu Met Glu Lys Met Gly Asp
 275 280 285
 His Leu Ala Leu Glu Asp Tyr Leu Thr Thr Asp Leu Val Glu
 290 295 300
 Thr Trp Leu Arg Asn Met Lys Thr Arg Asn Met Glu Val Phe
 305 310 315
 Phe Pro Lys Phe Lys Leu Asp Gln Lys Tyr Glu Met His Glu
 320 325
 Leu Leu Arg Gln Met Gly Ile Arg Arg Ile Phe Ser Pro Phe
 330 335 340
 Ala Asp Leu Ser Glu Leu Ser Ala Thr Gly Arg Asn Leu Gln
 345 350 355
 Val Ser Arg Val Leu Gln Arg Thr Val Ile Glu Val Asp Glu
 360 365 370
 Arg Gly Thr Glu Ala Val Ala Gly Ile Leu Ser Glu Ile Thr
 375 380 385
 Ala Tyr Ser Met Pro Pro Val Ile Lys Val Asp Arg Pro Phe
 390 395
 His Phe Met Ile Tyr Glu Glu Thr Ser Gly Met Leu Leu Phe
 400 405 410
 Leu Gly Arg Val Val Asn Pro Thr Leu Leu
 415 420

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Glu	Arg	Gly	Thr	Glu	Ala	Val	Ala	Gly	Ile	Leu	Ser	Glu	Ile	Thr
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Ala	Tyr	Ser	Met	Pro	Pro	Val	Ile	Lys	Val	Asp	Arg	Pro	Phe	His
				20					25					30
Phe	Met	Ile	Tyr	Glu	Glu	Thr	Ser	Gly	Met	Leu	Leu	Phe	Leu	Gly
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Arg	Val	Val	Asn	Pro	Thr	Leu	Leu							
				50										

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Ala	Tyr	Cys	Met	Pro	Pro	Val	Ile	Lys	Val	Asp	Arg	Pro	Phe	His
				20					25					30
Phe	Ile	Ile	Tyr	Glu	Glu	Met	Ser	Arg	Met	Leu	Leu	Phe	Leu	Gly
				35					40					45
Arg	Val	Val	Asn	Pro	Thr	Val	Leu							
				50										

<210> 11
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Glu	Lys	Gly	Thr	Glu	Ala	Ala	Gly	Ala	Met	Phe	Leu	Glu	Ala	Ile
1				5					10					15
Pro	Met	Ser	Ile	Pro	Pro	Glu	Val	Lys	Phe	Asn	Lys	Pro	Phe	Val
				20					25					30

Phe Leu Met Ile Glu Gln Asn Thr Lys Ser Pro Leu Phe Met Gly
35 40 45

Lys Val Val Asn Pro Thr Gln Lys
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<210> 12

<211> 53

<212> PRT

<213> Artificial Sequence

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<400> 12

Glu Lys Gly Thr Glu Ala Thr Gly Ala Pro His Leu Glu Glu Lys
1 5 10 15

Ala Trp Ser Lys Tyr Gln Thr Val Met Phe Asn Arg Pro Phe Leu
20 25 30

Val Ile Ile Lys Glu Tyr Ile Thr Asn Phe Pro Leu Phe Ile Gly
35 40 45

Lys Val Val Asn Pro Thr Gln Lys
50

<210> 13

<211> 56

<212> PRT

<213> Artificial Sequence

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<400> 13

Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr Ala Val Val Ile Ala
1 5 10 15

Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe Lys Ala Asn Arg
20 25 30

Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn Thr Ile Ile
35 40 45

Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
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<210> 14

<211> 53

<212> PRT

<213> Artificial Sequence

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Glu	Glu	Gly	Thr	Gln	Ala	Thr	Thr	Val	Thr	Thr	Val	Gly	Phe	Met
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Pro	Leu	Ser	Thr	Gln	Val	Arg	Phe	Thr	Val	Asp	Arg	Pro	Phe	Leu
				20					25					30

Phe	Leu	Ile	Tyr	Glu	His	Arg	Thr	Ser	Cys	Leu	Leu	Phe	Met	Gly
				35					40					45

Arg	Val	Ala	Asn	Pro	Ser	Arg	Ser
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<400> 15

Glu	Asp	Gly	Thr	Lys	Ala	Ser	Ala	Ala	Thr	Thr	Ala	Ile	Leu	Ile
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Ala	Arg	Ser	Ser	Pro	Pro	Trp	Phe	Ile	Val	Asp	Arg	Pro	Phe	Leu
				20					25					30

Phe	Phe	Ile	Arg	His	Asn	Pro	Thr	Gly	Ala	Val	Leu	Phe	Met	Gly
				35					40					45

Gln	Ile	Asn	Lys	Pro
				50

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Leu	Ala	Pro	Ser	Pro	Gln	Ser	Pro	Glu	Thr	Pro	Ala
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